FIG. 1∠

hlama5	domain VI Makricagsalcyrgprgpapillugiallgaarareeaggggpslhppyfnlaegariaasalcgeeapargsprpte 78
hlama5 mlama5	DLYCKLYGGPVAGGDPNOFIRCQYCDICTBANSNKAHBASNALDGTERWNGSPPLSRGLEYNEVNYTLDLGQVFHVAYVLIKFANSPRPDLWYLERSDROFFASSKRDCLERFGPQTLERLTRDDAAICTTEYSRIYPLENGEIVYSLYNGR 238
hlama5 mlama5	PGAMNESYSPILEBETKATNVRLAPLATUAGHLMGKALRDFVTRRYYSIKDISIGGRCVGHGAACDAKDPIDPFRLQCTCORTCDR.CCPGFNQOPWKPATANSANECOSCNCYGHATDCXYDPBVDRRAASOSLDGTYQGGGVCIDCQH 398
sanger hlama5 mlama5	T HTGWCERCLEGFYRSPWHELDS PHYCRACNCESDFTDGTCEDLTGRCYCRENESGERCDVCAEGFTGFPSCYPTPS-SSNDTREQYLEAGOIVNCDCSAAGTQGNACKNDRVGRCLCKENFGGTHCELCAPGFYGFGCQPCQCSCSPGVADDRCDDT 557 :
hlama5 mlama5	GOMCRYGFEGATODRCAPGYFHPPLOQLGGCSPAGTLPBGCDEAGRCLCQPEPAGPPROACTODPRGALDQLGGAGGLCRCRPGYTGARCOECSPGFHGFPSCVPGHAAGDPRSGCSCRPRVTGLRCDTCVPGAXNF 717
hlama5 mlama5	PYCEAGSCHPAGLAPUDPALPEAGVPCMCRAHVEGBSCDRCKEGFWGLSPSNPEGCTRCSCDLRGTLGGVAECOPGTGQCFCKPHVCGQACASCTGGFFGLDQADYFGCRSCKCDIGGALGGSCEPRTGVCRCRPWTGGPTCSEPARDHTLALE 877
hlama5 mlama5	LEEAATPEGHAVRFGENEERERFRIGTAQNAPVQPRIVARLALTSPDLFMLVFRYVNGGANSVSGRYSVREEGREAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
hlama5 mlama5	QOSGDNCLLYTHLPLOFPSAAGLEALCRODNSLERPCFFEQLSPSHPPLITCTGSDVDVQLQVAVPQPGRYALUVEYANEDARQEAPGRAPQQGLLSHAFGLYSTLCRGTARDTQDHLAVFHLDSEASVRLTAEQARFFLHGVTLVVFIEFSF 1197
hlama5 mlama5	EFVBERVSCISSHGAFORNSACLESRFFREPODILLRDCQVIPLEPGLELTHAQDLTPANSPAGEREPTAVDFDAEFTLIREPQATVFTHYPTGYAFLLHGYQBAHFTFPVEVLINAGRWQGHANASFCPHGYGGRTLWVCBQALLDVTHS 1357
hlama5 mlama5	domain IIID ELTVTVEVPEGRILMIDVYLVVPENVYSFGYLREEDDKSYDFISHGAAQGYHISPESSSIFFCRNAAASILSIFYNNGARFOCEPGGGCPCHAHVIGRDCSRCATGYWGFPNCRPCDCGARLCDELIGGCICPPRTIPPDCLLCQPGTF 1517
hlama5 mlama5	GCHPLYGCEECNCSGPG10ELTDPTCDTDSGQCKCRPNVTGRRCDTCSPGFHGYPRCREDCHEAGTAPGVCDPLTGQCYCKENVQGPKCDQCSLGTFSLDAANPKGCTRCFCFGAUERKRSSSYTRQBEVDMEGAWILSTDRQVVPHEKQPGTEMLRAD 1677
hlamas mlamas	IRHVPEAVPEAFPELYWQAPPSYLGDRYSSYGGTLRYELHSETQRGDVFVPMESRPDVVLQGNQMSITFLEPRYPFQHYHRQQLQLVEGNFRTETRNYVSREELMWVLASLEQLGRALFGGISSAVELRVALEVASPAGGALASNVELGLPASY 1837

FIG. 1B

3 235	233	24.	4 263	Y 279	1 29i	31:	αα 2,	89 W	33.55	365
HTTGPRCEICAPGEYGNALLPGNCTRCDCTPCGTEACDPHSGHCLCKAGYTGRRCDTGGRGFPCACGPAABSSECHPQSGQCHCRPGTMGPQCRECAPGYWGLDPGGGRCDPHTGRCNCPPGLSGERCDTCSQQHQVPVPGG	domain 1/11 PVGHSIHCEVCDHCVVLLLDDLERAGALLPAIHEQLRGINASSWAWARLHRLNASIADLQSQLRSPLGPRHETAQQLEVLEQQSTSLGQDARRLGGQAVGTRDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMSQTGHLGLANASAPSGEQLLRFTL	aeverlabmerrdegaabeaelaaroteleroeglesimeeroalatotedagegegingeroerigeroerigeroeglesednatioathaardtiasupakeeleriaasidgarteliormotes 	PAGSKLRLVBAREAHAQLOQLALNILSSIILDVNQDRLTQBAIEASNAYSRILOAVQAREDAAGQALQQADHTWATTVVRQQLYDRAQQLAANSTALEBAMLQBQRLGLVWAALQGARTQLRDVRAKKDQLEAHIQAAQANLAMDTDETSKKIAHAKAVA	domain G ARAQDTATRVQSQLQAMQENVERWQGQYEGLRGQDLGQAVLDAGHSVSTLEKTLPQLLAKLSILENRGVHNASLALSASIGRVRELIAQARGAASKVKVPMKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPSPGQGTEDRFVMYMGSRQATGDY	MGVSLRDKKVHWYQLGEAGPAVLSIDEDIGGFAAVSLDRTLQFGHMSVTVERQMIQETKGDFVARGALFARFTPPPPLARPGYRGCIEMDTLMEEVVSLYMFERTPQLDTAVDRPCARSKSTGDPMLTDGSYLDGTGFARI 	SPDSQISTTKRFEQELELVSYSGVLFFIKQQSQFLCLAVQBGSLVLLYDFGAGLKKAVPLQPPPPLTSASKALQVFLLGGSRKRVLVRVERATVYSVPQDNDLELADAYYLGGVPPDQLPPSLRMLFPTGGSVRGCVKGIKALGKYVDLKRLNTTGVSAG :-	CTADLLVGRAMTFHGHGFLRLALSNVAPLTGAVYSGFGFHSAQDSALLXYRASPDGLCQVSLQQGRVSLQLLRTEVKTQAGFABGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLLLGGLPESGTIYNFSGCISNVFVQRLLGPG 	RVEDLOONLGSVINUSTGCAPALOAOTPGLGPRGLOPRGFRENDPRHPACMLPPHLRTTRDSYOPGGSLSSHLEFVGILARHNWPSLSMHVLPRS-SRGLLLFTARLRPGSPSLALFLSNGHFVAQNEGLGTRLRAQSRQRSRPGRWHKVSVRRG 	KNRILLYTDGARANGOGGPHROHGOARHPOPHTLFVGGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAPTRANGVTPCILGPLEAGGGGTUFPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLQVTEKQVLLRADDGAGEFSTS	VTRPSVLCDGQWHRLAVMKSGNVLRLEVDAQSNHTVGPLIAAAAGAPAPLYLGGLPEPMAVQPMPPAYGGCMRLAVMKSPVAMTKSVEVHGAVGASGCPAA - -
Lama5 Lama5	lama5 Lama5	ama5	ama5 ama5	ama5 ama5	ama5 ama5	amas	ama5 ama5	ama5 ama5	ama5 ama5	ama5

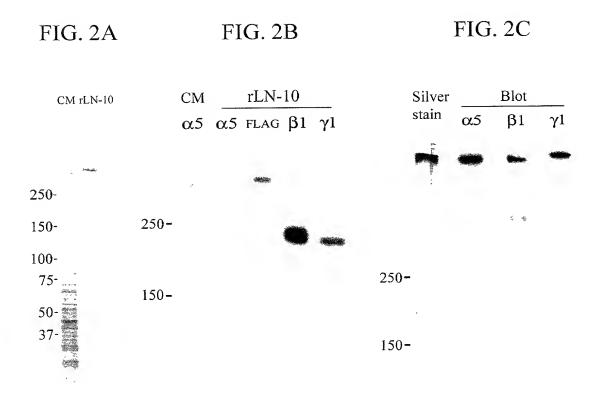


FIG. 3A

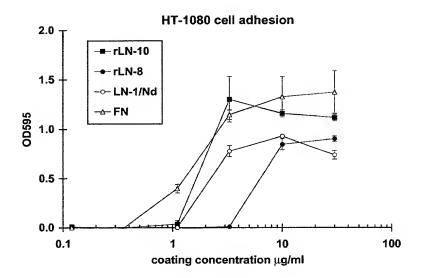


FIG. 3B

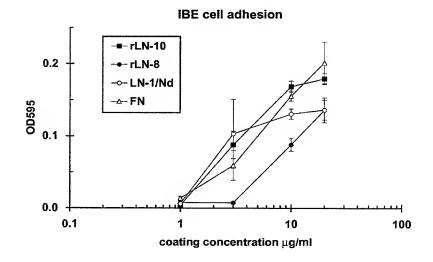


FIG. 3C

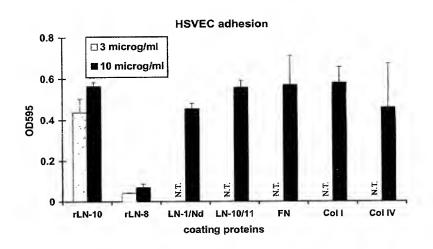


FIG. 4

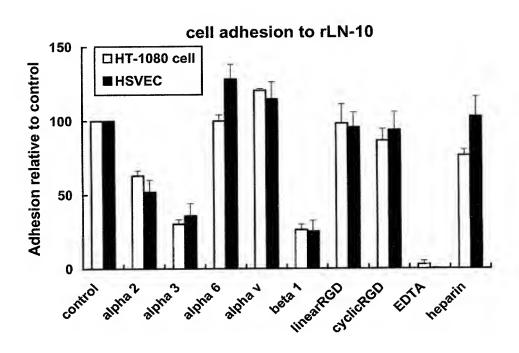


FIG. 5

